

**SCORE Search Results Details for Application 10573229 and Search Result 20090528\_121056\_us-10-573-229a-1.rge.**

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 21:47:12 ; Search time 916 Seconds  
(without alignments)  
101538.085 Million cell updates/sec

Title: US-10-573-229A-1  
Perfect score: 920  
Sequence: 1 tctgtagaggggaatggctg.....acccccaaagaaaccttcta 920

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14594359 seqs, 50548307366 residues

Total number of hits satisfying chosen parameters: 29188718

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_phg:\*  
4: gb\_pln:\*  
5: gb\_pri:\*  
6: gb\_rod:\*  
7: gb\_sts:\*  
8: gb\_syn:\*  
9: gb\_una:\*

10: gb\_vrl:\*  
 11: gb\_vrt:\*  
 12: gb\_inv:\*  
 13: gb\_mam:\*  
 14: gb\_bct:\*  
 15: gb\_htg1:\*  
 16: gb\_htg2:\*  
 17: gb\_htg3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	920	100.0	920	2	CS074575	CS074575 Sequence
	2	920	100.0	920	2	CS430220	CS430220 Sequence
	3	920	100.0	920	2	DJ044325	DJ044325 Identific
c	4	422.2	45.9	109238	5	AL133538	AL133538 Human DNA
	5	306	33.3	308	5	Z79429	Z79429 H.sapiens f
c	6	275	29.9	140243	15	AC067760	AC067760 Homo sapi
c	7	275	29.9	147659	15	AC015496	AC015496 Homo sapi
c	8	275	29.9	172212	5	AL136100	AL136100 Human DNA
	9	226.8	24.7	186029	16	AC169795	AC169795 Macaca mu
c	10	178.2	19.4	390	2	CS074841	CS074841 Sequence
c	11	178.2	19.4	390	2	DJ044524	DJ044524 Identific
c	12	176.6	19.2	390	2	CS430486	CS430486 Sequence
	13	122.6	13.3	561	2	AR612609	AR612609 Sequence
	14	122.6	13.3	561	2	AR799123	AR799123 Sequence
	15	122.6	13.3	561	2	DD052947	DD052947 SINGLE CO
	16	121.2	13.2	541	2	AR612608	AR612608 Sequence
	17	121.2	13.2	541	2	AR799122	AR799122 Sequence
	18	121.2	13.2	541	2	DD052946	DD052946 SINGLE CO
c	19	120	13.0	124409	5	AC069360	AC069360 Homo sapi
	20	120	13.0	165031	5	AC023850	AC023850 Homo sapi
c	21	114.2	12.4	769	7	BV595649	BV595649 S215P6066
c	22	112.6	12.2	92029	17	AL357492	AL357492 Homo sapi
	23	112.6	12.2	111182	5	AL359771	AL359771 Human DNA
c	24	111.8	12.2	171675	17	CU694921	CU694921 Sus scrof
	25	109.6	11.9	180602	5	AC010873	AC010873 Homo sapi
	26	109.6	11.9	186244	17	CU467509	CU467509 Sus scrof
c	27	109.6	11.9	197898	17	CT826373	CT826373 Sus scrof
	28	108	11.7	142859	5	AC008663	AC008663 Homo sapi
c	29	108	11.7	201170	15	AC022259	AC022259 Homo sapi
c	30	105.4	11.5	241493	17	AC213558	AC213558 Equus cab
	31	105	11.4	117916	17	AC225094	AC225094 Loxodonta
	32	105	11.4	123795	17	AC218085	AC218085 Loxodonta
c	33	105	11.4	198249	16	AC165117	AC165117 Bos tauru

	34	104.8	11.4	737	2	EA735231	EA735231	Sequence
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c	39	104.8	11.4	178050	5	AC142324	AC142324	Pan trogl
c	40	103.4	11.2	176644	5	AP002982	AP002982	Homo sapi
c	41	103.4	11.2	201190	15	AC022256	AC022256	Homo sapi
	42	103.2	11.2	183899	16	AC151854	AC151854	Papio ham
	43	103.2	11.2	206939	16	AC174979	AC174979	Bos tauru
c	44	103.2	11.2	208220	17	AC213940	AC213940	Equus cab
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ALIGNMENTS

RESULT 1

CS074575

LOCUS CS074575 920 bp DNA linear PAT 05-MAY-2005

DEFINITION Sequence 1 from Patent WO2005030250.

ACCESSION CS074575

VERSION CS074575.1 GI:63091182

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tuereci,O., Sahin,U., Helftenbein,G. and Schlueter,V.

TITLE Identification of tumour-associated cell surface antigens for  
diagnosis and therapy

JOURNAL Patent: WO 2005030250-A 1 07-APR-2005;  
Ganymed Pharmaceuticals AG (DE)

FEATURES

Location/Qualifiers

source

1. .920

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 920; DB 2; Length 920;

Best Local Similarity 100.0%; Pred. No. 7.4e-275;

Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60
Db	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60

Qy	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120
Db	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120
Qy	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Qy	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420
Db	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420
Qy	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Db	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Qy	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Db	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Qy	541	AAACCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
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Qy	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Db	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTGGGGAAGGAAAATCCCTACTGCCC	720
Db	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTGGGGAAGGAAAATCCCTACTGCCC	720
Qy	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Db	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Qy	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840
Db	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840

Qy 841 GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA 900  
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Db 841 GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA 900

Qy 901 ACCCCCAAAGAAACCTTCTA 920  
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Db 901 ACCCCCAAAGAAACCTTCTA 920

RESULT 2

CS430220

LOCUS CS430220 920 bp DNA linear PAT 19-OCT-2006

DEFINITION Sequence 1 from Patent WO2006100089.

ACCESSION CS430220

VERSION CS430220.1 GI:116291601

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Sahin,U., Tuereci,O., Koslowski,M., Helftenbein,G., Usener,D. and  
Schlueter,V.

TITLE Identification of surface-associated antigens for tumor diagnosis  
and therapy

JOURNAL Patent: WO 2006100089-A 1 28-SEP-2006;  
Ganymed Pharmaceuticals AG (DE)

FEATURES Location/Qualifiers

source 1. .920  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 920; DB 2; Length 920;  
Best Local Similarity 100.0%; Pred. No. 7.4e-275;  
Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60  
|||||

Db 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60

Qy 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120  
|||||

Db 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120

Qy 121 TGAGCCACTTTGGAAGCTGATCTTGAGCACCAAGCCCTTAGCTGGCTGCAGCCAC 180  
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Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTGACAAGGAA	300
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTGACAAGGAA	300
Qy	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420
Db	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420
Qy	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Db	421	TGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Qy	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Db	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Qy	541	AAACCCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
Db	541	AAACCCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
Qy	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Db	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCC	720
Db	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCC	720
Qy	721	CAAGAGCCAGCCCCGAACCCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
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Qy	901	ACCCCCAAAGAAACCTTCTA	920

Db 901 ACCCCCAAAGAAACCTTCTA 920

RESULT 3  
DJ044325  
LOCUS DJ044325 920 bp DNA linear PAT 26-OCT-2007  
DEFINITION Identification of Tumour-Associated Cell Surface Antigens for  
Diagnosis and Therapy.  
ACCESSION DJ044325  
VERSION DJ044325.1 GI:158737401  
KEYWORDS JP 2007506417-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 920)  
AUTHORS Herufutembain,G., Shuryuta,V., Sahin,U. and Tureci,O.  
TITLE Identification of Tumour-Associated Cell Surface Antigens for  
Diagnosis and Therapy  
JOURNAL Patent: JP 2007506417-A 1 22-MAR-2007;  
Ganymed Pharmaceuticals AG  
COMMENT OS Homo sapiens  
PN JP 2007506417-A/1  
PD 22-MAR-2007  
PF 23-SEP-2004 JP 2006527354  
PR 26-SEP-2003 DE 10344799.7  
PI geert herufutembain,volker shuryuta,ugur sahin,oezlem tureci  
CC  
FH Key Location/Qualifiers.  
FEATURES Location/Qualifiers  
source 1. .920  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
  
Query Match 100.0%; Score 920; DB 2; Length 920;  
Best Local Similarity 100.0%; Pred. No. 7.4e-275;  
Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60  
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Db 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60  
  
Qy 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120  
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Db 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120

Qy	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Db	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Db	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA	300
Qy	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420
Db	361	ATCATTGCTTCTGCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACG	420
Qy	421	TGGAGTGAAAACTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Db	421	TGGAGTGAAAACTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAA	480
Qy	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Db	481	TTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTA	540
Qy	541	AAACCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
Db	541	AAACCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATC	600
Qy	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Db	601	GAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTGGGGAAGGAAAATCCCTACTGCCC	720
Db	661	CAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTGGGGAAGGAAAATCCCTACTGCCC	720
Qy	721	CAAGAGCCAGCCCCGAACCCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Db	721	CAAGAGCCAGCCCCGAACCCAAGGCACAGCTTATACTGGCCCCGGGGCCTGGGGGGGCAC	780
Qy	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840
Db	781	GAAAACCTTGAAAAAGGGGCGCCTTCCCAGCTTCCCCGGGGGTAAGGGCTTTACCCCCCA	840
Qy	841	GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA	900
Db	841	GAGGGGGGGGGGAAAAATCCGAGTGGGATCTTTCCCAACCGCCGAAGACTAAAACCTTTAA	900



Qy 901 ACCCCCAAAGAAACCTTCTA 920  
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Db 901 ACCCCCAAAGAAACCTTCTA 920

## RESULT 4

AL133538/c

LOCUS AL133538 109238 bp DNA linear PRI 07-MAY-2008

DEFINITION Human DNA sequence from clone RP11-550N16 on chromosome 6q26-27  
Contains a CpG island, complete sequence.

ACCESSION AL133538

VERSION AL133538.16 GI:12666199

KEYWORDS HTG; CpG island.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 109238)

AUTHORS Wallis, J.

TITLE Direct Submission

JOURNAL Submitted (30-APR-2008) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk  
Clone requests: Geneservice (<http://www.geneservice.co.uk/>) and  
BACPAC Resources (<http://bacpac.chori.org/>)

COMMENT On Feb 5, 2001 this sequence version replaced gi:12655232.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: vega@sanger.ac.uk

-----

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)

This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>

RP11-550N16 is from the library RPCI-11.2 constructed by the group

of Pieter de Jong. For further details see <http://bacpac.chori.org/>  
VECTOR: pBACe3.6.

FEATURES	Location/Qualifiers
source	1..109238 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6" /map="q26-27" /clone="RP11-550N16" /clone_lib="RPCI-11.2"
misc_feature	109039 /note="Clone_left_end: RP1-263021"

ORIGIN

Query Match 45.9%; Score 422.2; DB 5; Length 109238;  
Best Local Similarity 94.5%; Pred. No. 3.1e-119;  
Matches 460; Conservative 0; Mismatches 23; Indels 4; Gaps 2;

[illegible]



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Qy 413 TTTTACGTGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCC 472  
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Db 121 TTTTACGTGGAGTGAAAACCTTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCC 180

Qy 473 CATGCCAATTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAA 532  
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Db 181 CATGCCAATTTCTCTGCTTCTGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAA 240

Qy 533 CGGGGGTAAACCCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAG 592  
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Db 241 CGGGGGTAAACCCCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAG 300

Qy 593 GTAGAATC 600  
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Db 301 GTANAATC 308

RESULT 6

AC067760/c

LOCUS AC067760 140243 bp DNA linear HTG 23-SEP-2000

DEFINITION Homo sapiens chromosome 2 clone RP11-309K2 map 2, WORKING DRAFT  
SEQUENCE, 27 unordered pieces.

ACCESSION AC067760

VERSION AC067760.2 GI:10280923

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 140243)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 2, clone RP11-309K2

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 140243)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,  
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,  
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,  
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,  
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Sep 23, 2000 this sequence version replaced gi:7651809.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L9986

Center clone name: 309\_K\_2

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 128933 bases at least Q40

Consensus quality: 134958 bases at least Q30

Consensus quality: 136879 bases at least Q20

Insert size: 148000; agarose-fp

Insert size: 137643; sum-of-contigs

Quality coverage: 3.5 in Q20 bases; agarose-fp

Quality coverage: 3.8 in Q20 bases; sum-of-contigs

-----.

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 27 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

*	1	4248: contig of 4248 bp in length
*	4249	4348: gap of 100 bp
*	4349	5605: contig of 1257 bp in length
*	5606	5705: gap of 100 bp
*	5706	7181: contig of 1476 bp in length
*	7182	7281: gap of 100 bp
*	7282	9012: contig of 1731 bp in length
*	9013	9112: gap of 100 bp

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*      9113      10509: contig of 1397 bp in length
*      10510     10609: gap of 100 bp
*      10610     13120: contig of 2511 bp in length
*      13121     13220: gap of 100 bp
*      13221     15323: contig of 2103 bp in length
*      15324     15423: gap of 100 bp
*      15424     17407: contig of 1984 bp in length
*      17408     17507: gap of 100 bp
*      17508     20878: contig of 3371 bp in length
*      20879     20978: gap of 100 bp
*      20979     22666: contig of 1688 bp in length
*      22667     22766: gap of 100 bp
*      22767     26227: contig of 3461 bp in length
*      26228     26327: gap of 100 bp
*      26328     29552: contig of 3225 bp in length
*      29553     29652: gap of 100 bp
*      29653     33144: contig of 3492 bp in length
*      33145     33244: gap of 100 bp
*      33245     35959: contig of 2715 bp in length
*      35960     36059: gap of 100 bp
*      36060     40873: contig of 4814 bp in length
*      40874     40973: gap of 100 bp
*      40974     46108: contig of 5135 bp in length
*      46109     46208: gap of 100 bp
*      46209     50453: contig of 4245 bp in length
*      50454     50553: gap of 100 bp
*      50554     54780: contig of 4227 bp in length
*      54781     54880: gap of 100 bp
*      54881     60935: contig of 6055 bp in length
*      60936     61035: gap of 100 bp
*      61036     68604: contig of 7569 bp in length
*      68605     68704: gap of 100 bp
*      68705     75243: contig of 6539 bp in length
*      75244     75343: gap of 100 bp
*      75344     81214: contig of 5871 bp in length
*      81215     81314: gap of 100 bp
*      81315     87663: contig of 6349 bp in length
*      87664     87763: gap of 100 bp
*      87764     94389: contig of 6626 bp in length
*      94390     94489: gap of 100 bp
*      94490     105834: contig of 11345 bp in length
*     105835     105934: gap of 100 bp
*     105935     125401: contig of 19467 bp in length
*     125402     125501: gap of 100 bp
*     125502     140243: contig of 14742 bp in length.

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	/note="assembly_fragment"
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Best Local Similarity 100.0%; Pred. No. 2.7e-73;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60
Db	51788	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	51729
Qy	61	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	120
Db	51728	CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC	51669
Qy	121	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	180
Db	51668	TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC	51609
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	240
Db	51608	AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT	51549
Qy	241	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG	275
Db	51548	GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG	51514

RESULT 7  
AC015496/c  
LOCUS AC015496 147659 bp DNA linear HTG 16-MAR-2000  
DEFINITION Homo sapiens clone RP11-21E5, WORKING DRAFT SEQUENCE, 7 unordered pieces.  
ACCESSION AC015496



VERSION AC015496.3 GI:7249030  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 147659)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 TITLE Homo sapiens, clone RP11-21E5  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 147659)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
 Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,  
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,  
 Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
 Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,  
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 Lehoczkyl,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,  
 McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,  
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 COMMENT On Mar 16, 2000 this sequence version replaced gi:6553986.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L3993  
 Center clone name: 21\_E\_5  
 ----- Summary Statistics  
 Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 129300 bases at least Q40  
 Consensus quality: 140951 bases at least Q30  
 Consensus quality: 145175 bases at least Q20  
 Insert size: 146000; agarose-fp  
 Insert size: 147059; sum-of-contigs

Quality coverage: 5.8 in Q20 bases; agarose-fp  
 Quality coverage: 5.7 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 7 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\*       1       2851: contig of 2851 bp in length  
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 \*       6912       7011: gap of 100 bp  
 \*       7012       13475: contig of 6464 bp in length  
 \*       13476       13575: gap of 100 bp  
 \*       13576       29402: contig of 15827 bp in length  
 \*       29403       29502: gap of 100 bp  
 \*       29503       54805: contig of 25303 bp in length  
 \*       54806       54905: gap of 100 bp  
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misc_feature	7012. .13475 /note="assembly_fragment"
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vector\_side:right"

ORIGIN

Query Match 29.9%; Score 275; DB 15; Length 147659;  
Best Local Similarity 100.0%; Pred. No. 2.8e-73;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60  
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Db 41178 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 41119

Qy 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120  
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Qy 121 TGAGCCACTTTGGAAGCTGATCTTGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180  
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Db 41058 TGAGCCACTTTGGAAGCTGATCTTGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 40999

Qy 181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240  
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Db 40998 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 40939

Qy 241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 275  
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Db 40938 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 40904

RESULT 8  
AL136100/c  
LOCUS AL136100 172212 bp DNA linear PRI 06-MAY-2008  
DEFINITION Human DNA sequence from clone RP11-534P19 on chromosome 6 Contains  
a pseudogene similar to zinc finger proteins, complete sequence.  
ACCESSION AL136100  
VERSION AL136100.12 GI:11322762  
KEYWORDS HTG; zinc finger.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 172212)  
AUTHORS Bird,C.  
TITLE Direct Submission  
JOURNAL Submitted (30-APR-2008) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk  
Clone requests: Geneservice (<http://www.geneservice.co.uk/>) and BACPAC Resources (<http://bacpac.chori.org/>)  
COMMENT On Nov 23, 2000 this sequence version replaced gi:11139882.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: vega@sanger.ac.uk  
-----  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>  
RP11-534P19 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://bacpac.chori.org/>  
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ORIGIN

Query Match 29.9%; Score 275; DB 5; Length 172212;  
Best Local Similarity 100.0%; Pred. No. 2.8e-73;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CACTTGGTGAGAAACCGATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120  
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Qy 121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180  
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Db 93204 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 93145

Qy 181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240  
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Db 93144 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 93085

Qy 241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 275  
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RESULT 9

AC169795

LOCUS AC169795 186029 bp DNA linear HTG 12-NOV-2005

DEFINITION Macaca mulatta clone CH250-283M17, WORKING DRAFT SEQUENCE, 3 ordered pieces.

ACCESSION AC169795

VERSION AC169795.2 GI:82174563

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLLTOP.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 186029)

AUTHORS Muzny,D.M., Abraham,K.K., Abulimiti,A., Adams,C.Q., Aduba,G., Allen,C.C., Alsbrooks,S.L., Anosike,U.S., Archer,P.M., Arredondo,H.H., Attaway,T., Bandaranaike,D.P., Bangura,L., Barton,S.R., Bell,A.V., Bell,S.N., Beraducci,A.R., Bickham,C., Biswalo,K., Blyth,P.R., Buhay,C.J., Canada,A., Cardenas,V.,

Carter,K., Chacko,J., Chandrabose,M.N., Chavez,A., Chavez,D.,  
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 Dao,M.D., Davila,M., Davis,C., Davy-Carroll,L., Del fierro,P.,  
 Demen,R., Denson,S., Ding,Y., Dinh,H.H., Donlin,J.E.,  
 Dugan-Rocha,S., Dunn,A.M., Durbin,K.J., Ebong,V.E., Egan,A.,  
 Espinosa,V.C., Fa,M., Fernandez,S., Fernando,P.R., Ferrer,A.R.,  
 Flagg,N., Forbes,L.D., Fowler,R.G., Fu,Q., Fuh,E., Gabisi,R.A.,  
 Ganardhanan,M., Ganer,J., Garcia iii,R.M., Garcia,A.M.,  
 Garcia,S.M., Garner,T.T., Ghose,S., Gingras,M.,  
 Gonzalez-Garay,M.L., Guevara,W.V., Haaland,W.C., Haeberlen,K.A.,  
 Hagans,B.J., Hall,O., Hamid,H., Hamilton,K.A., Hampton,O.A.,  
 Harbes,B.A., Harris,R.A., Havlak,P., Hawes,A.C., Hawkins,E.S.,  
 Haynes,S.J., Hemphill,L., Hernandez,J., Hines,S., Hirani,K.,  
 Hitchens,M.E., Hodgson,A.V., Hogues,M.E., Holder,M., Hollins,B.,  
 Howell,L.L., Hulyk,S.W., Hume,J., Jackson,A., Jackson,L.R.,  
 Jacob,S.K., Jhangiani,S.N., Jiang,H., Johnson,B., Johnson,R.,  
 Joshi,V., Joy,C., Kaikai,F.B., Kalafus,K.J., Kalu,J.B., Kang,Y.,  
 Keebler,J., Khan,Z.M., Kidwai,S., King,L.M., Kisamo,H., Kovar,C.L.,  
 Kowis,A.N., Kowis,C.R., Lago,L.A., Lago,M.T., Lai,C., Lara,F.,  
 Le,T.T., Lee,S.L., Lee,T.W., Legall iii,F.H., Lemon,S.J.,  
 Lewis,L.R., Li,B., Li,Y., Li,Z., Linnell,M.A., Liu,J., Liu,W.,  
 Liu,Y., Liu,Y., Liyanage,D., London,P., Lopez,J., Lorensuhewa,L.M.,  
 Lozado,R.J., Luc,T., Madu,R.C., Maheshwari,M., Maheshwari,R.,  
 Malloy,K., Mansouri,D.L., Martinez,E., Matejkova,P., Mathew,T.,  
 Mccauley,S.K., Mcpherson,J.D., Mercado,C., Mercado,I.C.,  
 Metzker,M.L., Millin,A., Milosavljevic,A., Morgan,M.B., Morris,S.,  
 Munidasam,M., Murray,D.D., Muzny,D.M., Nazareth,L.V., Ngo,D.N.,  
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 Onyenekwe,J., Parish,B.J., Parker,D.N., Parra,A.A., Pasternak,S.,  
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 Perez,Y.Y., Pham,T.L., Player,E.J., Primus,E.L., Pu,L., Puazo,M.,  
 Purkiss,C., Qin,X., Quiroz,J.B., Rabata,D., Rachlin,E.K., Ren,Y.,  
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 Savery,G.G., Scherer,S.E., Schneider,B.W., Sebasigari,R.,  
 Sexton,M.M., Shen,H., Shen,Y., Sisson,I., Sneed,A.J., Sodergren,E.,  
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 Thelus,R., Thomas,N., Thorn,R.D., Thornton,R.D., Tong,M.Y.,  
 Trejos,Z.Y., Usmani,K., Vargo,C.E., Vattathil,S., Vega,R.A.,  
 Villasana,D., Volkov,A., Walker,D.L., Wang,Q., Wang,S.,  
 Warren,J.T., Watt,J.E., Wei,X., Wheeler,D.A., White,C.S., Williams  
 jr,R.L., Williams,A.C., Williams,G.A., Williams,J.D., Wilson,K.,  
 Woodworth,J.R., Worley,K.C., Wright,R.A., Wu,J., Wu,W., Yakub,S.,  
 Yerrapragada,S., Yu,F., Yuan,D.T., Yuan,Y., Zhang,J., Zhang,L.,  
 Zhang,Z., Zhou,J., Zhu,Y., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 186029)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (12-OCT-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 186029)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (12-NOV-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 12, 2005 this sequence version replaced gi:77539482.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help.tmc.edu](mailto:hgsc-help.tmc.edu)

----- Project Information

Center project name: LDVL

Center clone name: CH250-283M17

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye:100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 186011 bases at least Q40

Consensus quality: 186345 bases at least Q30

Consensus quality: 186634 bases at least Q20

Estimated insert size: 205029; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html))

\* The sequence data in this record represents an 'enhanced' version

\* of a Phase 2 submission. The indicated order and orientation of

\* each sequence has been established using one or more of the

\* following: read-pair data from individual subclones, overlaps

\* with neighboring clones, alignment with available reference

\* sequence (e.g., human), and/or confirmation by PCR testing.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 3 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submittor.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

\* 1 54276: contig of 54276 bp in length

\* 54277 54376: gap of 100 bp

\* 54377 104140: contig of 49764 bp in length

\* 104141 104340: gap of 200 bp

\* 104341 186029: contig of 81689 bp in length.

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misc_feature	104341..186029 /note="assembly_name:Contig40"

ORIGIN

Query Match	24.7%;	Score 226.8;	DB 16;	Length 186029;
Best Local Similarity	91.3%;	Pred. No. 3.1e-58;		
Matches	252;	Conservative 0;	Mismatches 22;	Indels 2; Gaps 1;
Qy	1	TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60	
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Qy	121	TGAGCCACTTTGGAAGCTGATCTTGAGCACCA--GTCAAGCCCTTAGCTGGCTGCAGCC	178	
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Qy	179	ACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAA	238	
Db	152532	CCAGCCAACAATAAGACTGCAACCTCCTGGGGAATCCTGAGCCAGAATCCCCTGGCTAAA	152591	
Qy	239	TTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAA	274	
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RESULT 10  
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LOCUS CS074841 390 bp DNA linear PAT 05-MAY-2005  
DEFINITION Sequence 267 from Patent WO2005030250.



Query Match 19.4%; Score 178.2; DB 2; Length 390;  
Best Local Similarity 93.5%; Pred. No. 2e-43;  
Matches 186; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy	388	AGCATCACCCACTTCCCCAGAACCTTTTTTTACGTGGAGTGAAAACTTTAAGGGGCTGTCC	447
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Query Match 13.3%; Score 122.6; DB 2; Length 561;  
Best Local Similarity 69.6%; Pred. No. 4.7e-26;  
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy	2	CTGTAGAGGGGAATGGCTGCTGTGTTCATGGGGGTGCATGAGCAGCCCCAGTGGAGAGGTGC	61
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Qy	62	ACTTGGTGAGAAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGTC-----	114
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Qy	115	-----TGAGACTGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGC	167
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Qy	168	TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC	227
Db	381	TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC	440
Qy	228	CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA	276
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LOCUS       AR799123                561 bp    DNA             linear       PAT 05-APR-2006
DEFINITION  Sequence 108 from patent US 7014997.
ACCESSION   AR799123
VERSION     AR799123.1   GI:91151193
KEYWORDS    .
SOURCE      Unknown.
   ORGANISM Unknown.
             Unclassified.
REFERENCE   1   (bases 1 to 561)

```

AUTHORS Knoll,J.H.M. and Rogan,P.K.  
TITLE Chromosome structural abnormality localization with single copy probes  
JOURNAL Patent: US 7014997-A 108 21-MAR-2006;  
The Children's Mercy Hospital; Kansas City, MO;  
US;

FEATURES Location/Qualifiers  
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ORIGIN

Query Match 13.3%; Score 122.6; DB 2; Length 561;  
Best Local Similarity 69.6%; Pred. No. 4.7e-26;  
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

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RESULT 15

DD052947  
LOCUS DD052947 561 bp DNA linear PAT 04-NOV-2005  
DEFINITION SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME.  
ACCESSION DD052947  
VERSION DD052947.1 GI:92688538  
KEYWORDS JP 2004523201-A/108.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 561)  
 AUTHORS Joan,K.H.M., Rogan,P.K. and Kazarro,P.M.  
 TITLE SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING  
 JOURNAL Patent: JP 2004523201-A 108 05-AUG-2004;  
 KNOLL H JOAN,PETER K ROGAN

COMMENT OS Homo sapiens  
 PN JP 2004523201-A/108  
 PD 05-AUG-2004  
 PF 15-MAY-2001 JP 2001585298  
 PR 16-MAY-2000 US 09/573080,14-MAY-2001 US 09/854867 PI  
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## ORIGIN

Query Match 13.3%; Score 122.6; DB 2; Length 561;  
 Best Local Similarity 69.6%; Pred. No. 4.7e-26;  
 Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61  
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